

FIG.1

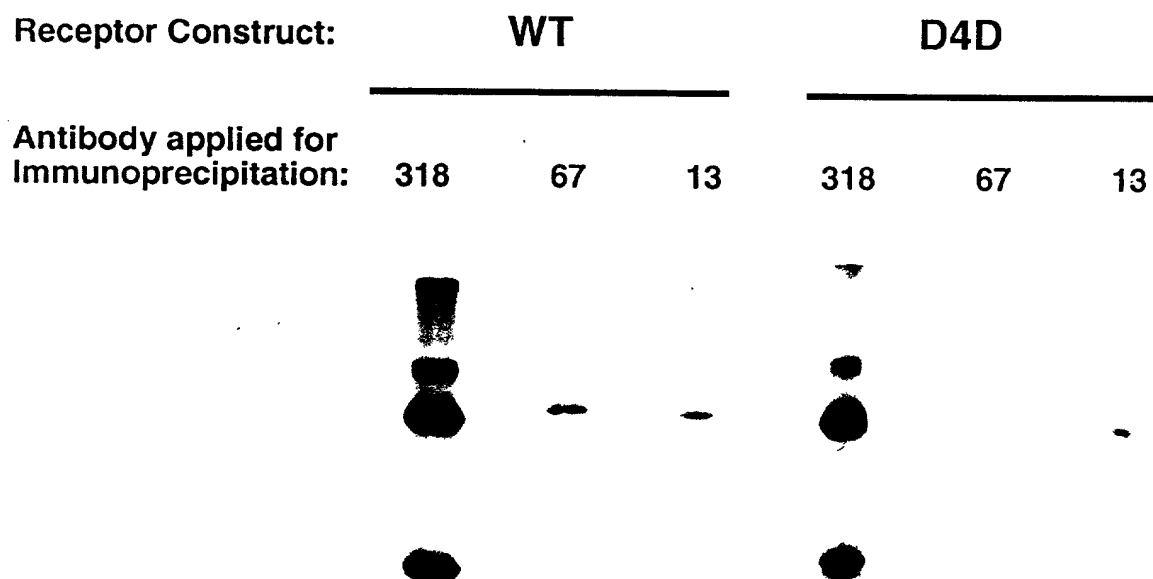


FIG. 2A

1
gcgagcgcag cggagcctgg agagaaggcg ctgggctgcg agggcgcgag ggcgcgaggg cagggggcaa cgggaccccg
81 cccgcaccc atg gcg ccc gtc gcc gtc tgg gcc gcg ctg gcc gtc gga ctg gag ctc tgg gct gcg
Met Ala Pro Val Ala Val Trp Ala Ala Leu Ala Val Gly Leu Glu Leu Trp Ala Ala
147 -22
gcg cac gcc ttg ccc gcc cag gta gca ttt aca ccc tac gcc ccg gag ccc ggg agc aca tgc cgg
Ala His Ala Leu Pro Ala Gln Val Ala phe Thr Pro Tyr Ala pro Glu Pro Gly Ser Thr Cys Arg
213 -1 +1
ctc aga gaa tac tat gac cag aca gct cag atg tgc tgc agc aaa tgc tgc ccg ggc caa cat gca
Leu Arg Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala
279
aaa gtc ttc tgt acc aag acc tcg gac acc gtg tgt gac tcc tgt gag gac agc aca tac acc cag
Lys Val phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp Ser Thr Tyr Thr Gln
345
ctc tgg aac tgg gtt ccc gag tgc ttg agc tgt ggc tcc cgc tgt agc tct gac cag gtg gaa act
Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr
411
caa gcc tgc act cgg gaa cag aac cgc atc tgc acc tgc agg ccc ggc tgg tac tgc gcg ctg agc
Gln Ala Cys Thr Arg Glu Gln Asn Arg ile Cys Thr Cys Arg pro Gly Trp Tyr Cys Ala Leu Ser
477
aag cag gag ggg tgc cgg ctg tgc gcg ccg ctg cgc aag tgc cgc ccg ggc ttc ggc gtg gcc aga
Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg Pro Gly phe Gly Val Ala Arg
543
cca gga act gaa aca tca gac gtg tgc aag ccc tgc gcc ccg ggg acg ttc ttc aac acg act
Pro Gly Thr Glu Thr Ser Asp Val Val Cys Lys Pro Cys Ala Pro Gly Thr phe Ser Asn Thr Thr
609
tca tcc acg gat att tgc agg ccc cac cag atc tgt aac gtg ggc atc ccc ggg aat gca agc
Ser Ser Thr Asp Ile Cys Arg Pro His Gln ile Cys Asn Val Val Ala ile Pro Gly Asn Ala Ser
675
atg gat gca gtc tgc acg tcc acg tcc ccc acc cgg agt atg gcc cca ggg gca gta cac tta ccc
Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser Met Ala pro Gly Ala Val His Leu Pro
741

FIG. 2B

cag cca gtg tcc aca cga tcc caa cac acg cag cca act cca gaa ccc agc act gct cca agc acc
 Gln Pro Val Ser Thr Arg Ser Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr
 807
 tcc ttc ctg ctc cca atg ggc ccc agc ccc cca gct gaa ggg agc act ggc gac ttc gct ctt cca
 Ser Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly Asp Phe Ala Leu Pro
 873
 gtt gga ctg att gtg ggt gtg aca gcc ttg ggt cta cta ata gga gtg gtg aac tgt gtc atc
 Val Gly Leu Ile Val Gly Val Thr Ala Leu Gly Leu Leu Ile Ile Gly Val Val Asn Cys Val Ile
 939
 atg acc cag gtg aaa aag aag ccc ttg tgc ctg cag aga gaa gcc aag gtg cct cac ttg cct gcc
 Met Thr Gln Val Lys Lys Lys Pro Leu Cys Leu Gln Arg Glu Ala Lys Val Pro His Leu Pro Ala
 1005
 gat aag gcc cgg ggt aca cag ggc ccc gag cag cag cag ctg ctg atc aca gcg ccg agc tcc agc
 Asp Lys Ala Arg Gly Thr Gln Gly Pro Glu Gln Gln His Leu Leu Ile Thr Ala Pro Ser Ser Ser
 1071
 agc agc tcc ctg gag agc tgc gcc agt gcg ttg gac aga agg gcg ccc act cgg aac cag cca cag
 Ser Ser Ser Leu Glu Ser Ser Ala Ser Ala Leu Asp Arg Arg Ala Pro Thr Arg Asn Gln Pro Gln
 1137
 gca cca ggc gtg gag gcc agt ggg gcc gcg gag gcc cgg gcc agc acc ggg agc tca gat tct tcc
 Gly Ala Gly Glu Ala Arg Ala Ser Thr Gly Ser Ser Asp Ser Ser Pro Gly Gly His Gly Thr Gln
 1203
 ctt ggt ggc cat ggg acc cag gtc aat gtc acc tgc atc gtg aac gtc tgt agc agc tct gac cac
 Ala Pro Gly Val Glu Ala Ser Val Asn Val Thr Cys Ile Val Asn Val Cys Ser Ser Ser Asp His
 1269
 agc tca cag tgc tcc tcc caa gcc agc tcc aca atg gga gac aca gat tcc agc ccc tcg gag tcc
 Ser Ser Gln Cys Ser Ser Gln Ala Ser Ser Thr Met Gly Asp Thr Asp Ser Ser Pro Ser Glu Ser
 1335
 ccg aag gac gag cag gtc ccc ttc tcc aag gag gaa tgt gcc ttt cgg tca cag ctg gag acg cca
 Pro Lys Asp Glu Gln Val Pro Phe Ser Lys Glu Glu Cys Ala Phe Arg Ser Gln Leu Glu Thr Pro
 1401
 gag acc ctg ctg ggg agc acc gaa gag aag ccc ctg ccc ctt gga gtg cct gat gct ggg atg aag
 Glu Thr Leu Leu Gly Ser Thr Glu Glu Lys Pro Leu Pro Leu Gly Val Pro Asp Ala Gly Met Lys
 1467
 ccc agt taa ccaggccggt gtgggctgtg tcgtagccaa ggtgggtga gccctggcag gatgacctg cgaagggg
 Pro Ser End
 439

TRANSMEMBRANE

DOMAIN

FIG. 3

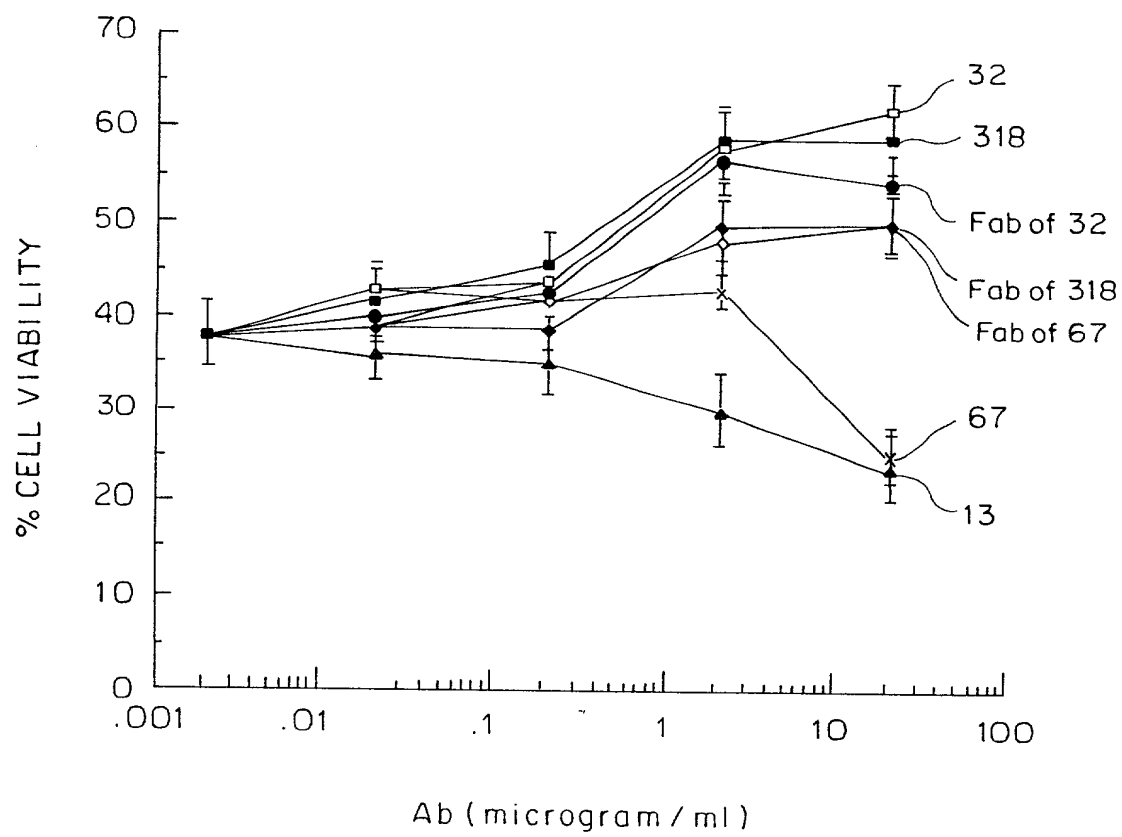


FIG. 4

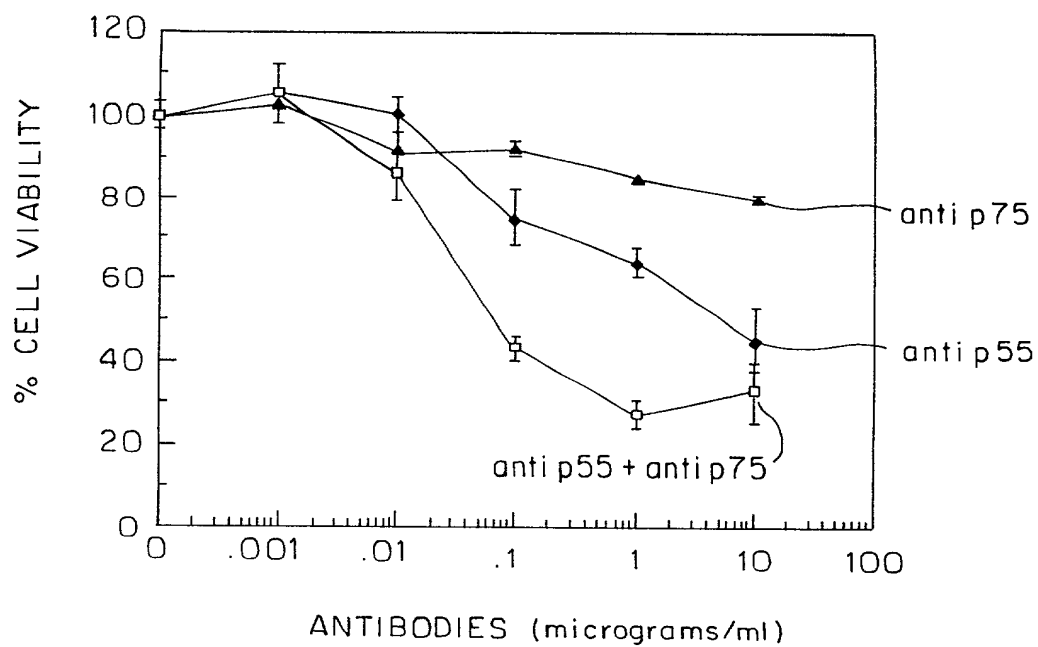


FIG. 5

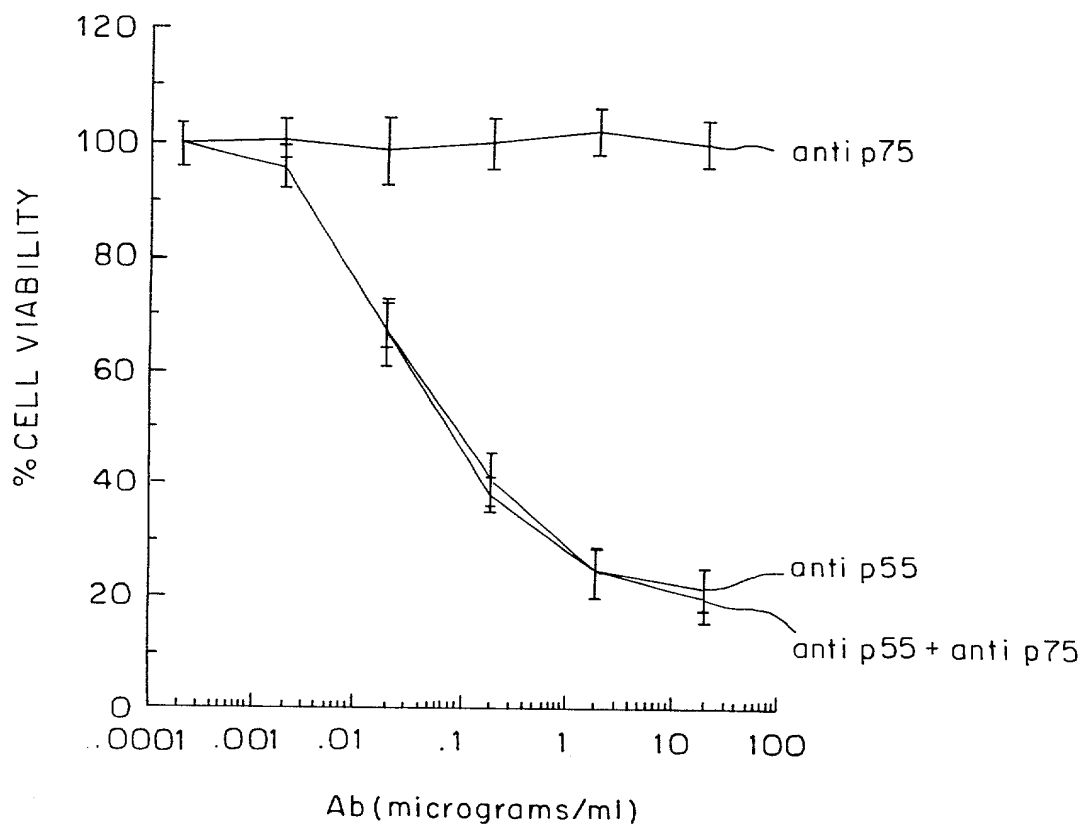


FIG. 6

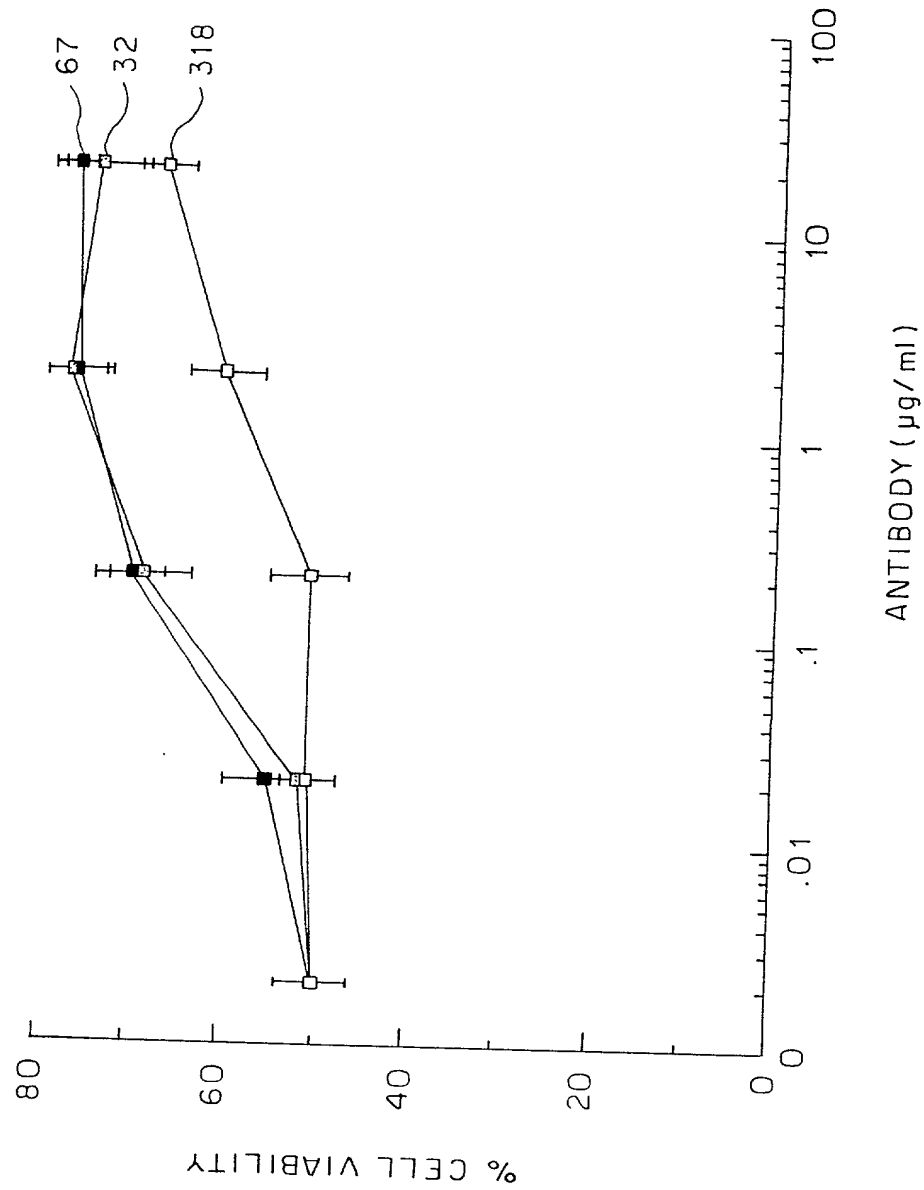


FIG. 7

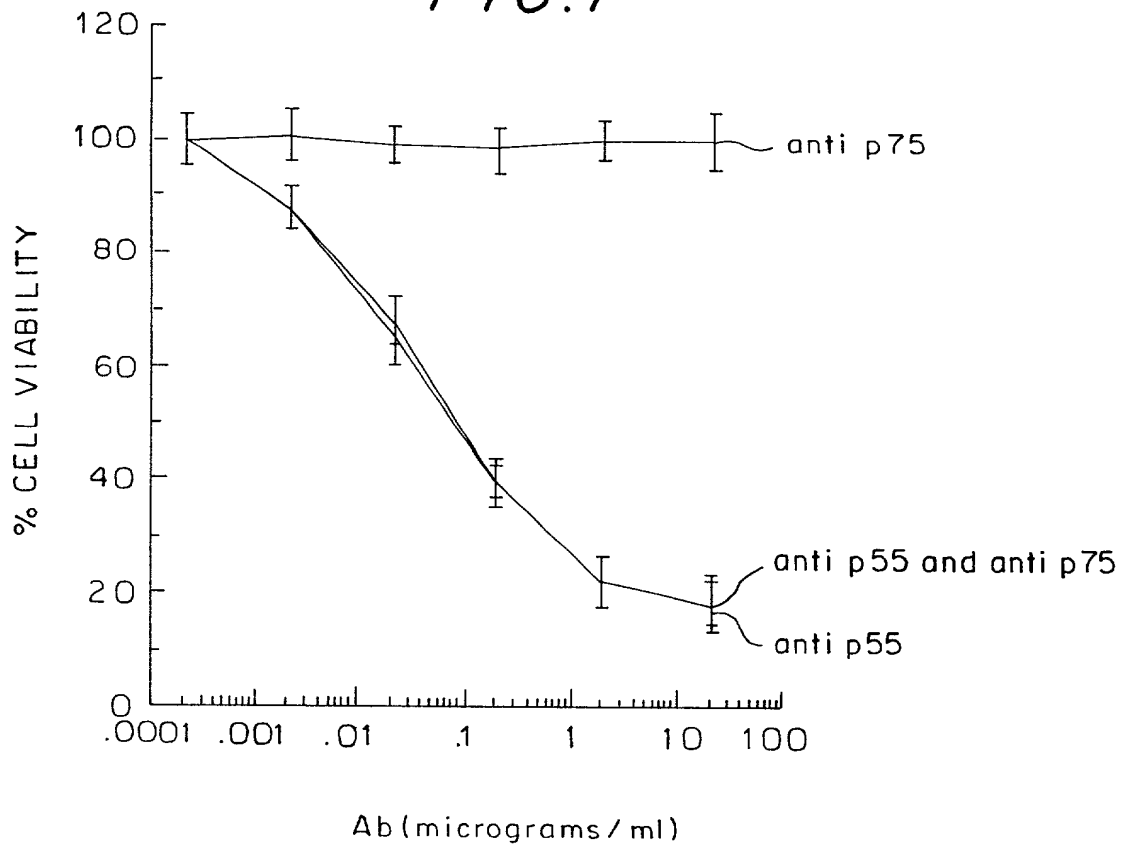


FIG. 8

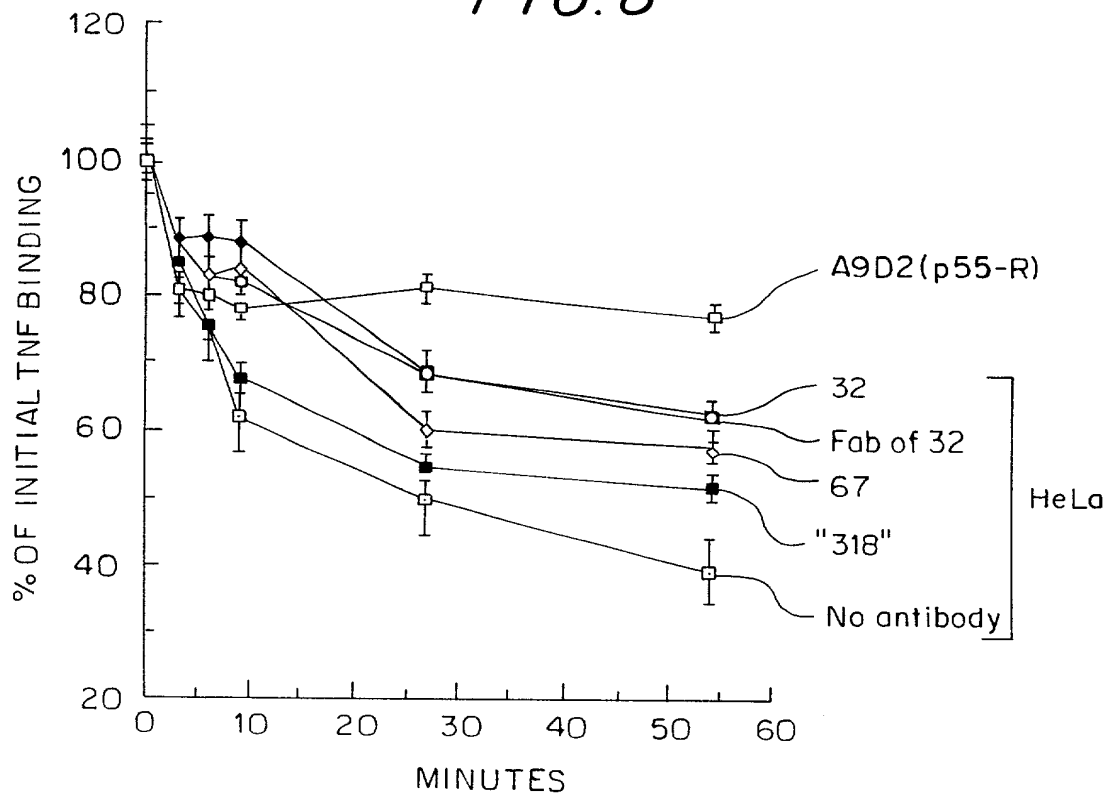


FIG.9

hu p55 TNF-R (3-42)	VCPQGGKYIHPQNN---SICCC-TKCHKGTYLYND---CPGPGQDTDCR
hu p75 TNF-R (39-76)	TCRLREYD-QTA---QMCC-SKCSFGQHAKVF---CTKTS-DTVCD
hu FAS (31-67)	QNLGLH-HDGGQF---CH-KPCPPGERKARD---CTVNGDEPDCV
hu NGF-R (3-37)	ACPTGLYTHSGE---CC-KACNLGEGVAQP---CGA-NQTVCE
hu CDW40 (25-60)	ACREKQYLINSQ---CC-SLCPGQKLVSD---CTEF-TETECCL
rat Ox40 (25-60)	NCVKDTYPSGHK---CC-RECPGCHGMVSR---CDHT-RDITVCH
hu p55 TNF-R (43-86)	ECESGSFTASEHHL-RHCLLSC-SKCRKENGQVEISSCTVD-RDITVCG
hu p75 TNF-R (77-119)	SCEDSTYTQLWNWV-PECLSCGSRCSDD--QVETQACTRE-QNRICCT
hu FAS (68-112)	ECQEGKEYTDKAHFSSKRRRC-RLCDGHLGVEINCTRT-QNTKCR
hu NGF-R (38-80)	PCLDSTVSSDVVSATEPCPKPC-TECVGLQSHSAP--CVEA-DDAVCR
hu CDW40 (61-104)	PCGESEFLDWTWRETN-CHQH-KYCDPNLGLRVQKGTSE-TDTICT
rat Ox40 (61-104)	PC-EPGFYNEAVNY-DTCKQC-TQCNRHRSSELKQNTPT-EDTVCQ
hu p55 TNF-R (87-126)	-CRKNQVRHYWSENLFQCFNC---SLCLHGT-VHLSQCEK-QNTVC-
hu p75 TNF-R (120-162)	-CRPGWYCA--LSKQEGCRLCAPLRKCRPGFGVARPGTET-SDVVCK
hu FAS (113-149)	-CKPNFFCN--STVCEHCDPC---TKCEHGI-IKE-CTLT-SNTKC-
hu NGF-R (81-119)	-CAYGYQD---ETTGRCEAC---RVCEAGSGLVFSQQDK-QNTVCE
hu CDW40 (105-144)	-CEEGWHC-----TSEACESCVLHRSCLSPGFGVKQIATGV-SDTICE
rat Ox40 (105-123)	-CRPGTQP-----RQDS-----SHKLGVDD-----CV
hu p55 TNF-R (127-155)	TCHAGFFLR--ENE---CVSC-SNCKKSL-----ECTK-----LC-
hu p75 TNF-R (163-201)	ECAPGTFSTTSST-DICRPH-QICN-----VVA--IPGNASMDAVCT
hu NGF-R (120-161)	ECFDGTYSDAHHV-DPCLPQC-TVCEDETERQLR--ECTRW-ADAECE
hu CDW40 (145-186)	ECFVGFFSNVSSAF-EKCHP--TSCETKDLVVQ--QAGTNKTDVCCG
rat Ox40 (124-164)	PCFPFGHFSFGSHQ---ACKPW-TNCTLSGKQIR--HPASNSLDTVCE